Atelier Inra-Cirad Idéotypes fruitiers
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IDEOFRUIT WP3

GENETICS AND FUNCTIONAL GENOMICS OF FRUIT QUALITY TRAITS AND PLANT DEFENCE

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WP3. Genetics and functional genomics of fruit quality traits and plant defence

1. Specific objectives

To acquire knowledge of the genetics and genomics of traits related to fruit quality and resistance to pests and diseases (**Banana** and **Peach**)

2. Methodology

For cooking **Banana**, the genetic diversity will be characterized using genome-wide distributed molecular markers.

Candidate genes related to starch metabolism will be identified and sequenced, assuming that this process is closely related to fruit quality traits. The most appropriate candidate genes will be selected based on their expression pattern during fruit development and ripening of different and contrasted **Banana** varieties.

Candidate genes involved in the constitutive expression of defence-related genes of **Banana** to *Mycosphaerella spp.* will be identified, taking help from the whole sequence of the **Banana** A genome released in 2010.

For **Peach**, the gene involved in the biosynthesis of 3,5-dicaffeoylquinic acid, a phenolic compound involved in the resistance to *Myzus persicae* will be characterized, first isolating and sequencing the enzyme involved in the biosynthesis. QTL of biochemical components and traits linked to resistance of **Peach** to *Monilinia* spp. will be mapped.

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WP3. Genetics and functional genomics of fruit quality traits and plant defence

3. Planned activities

Bananas and plantains

3.1. Characterization of the genetic diversity of cooking banana using genome-wide distributed molecular markers

3.2. Identification of candidate genes involved in the determination of quality traits (metabolic pathways, sequence and allelic diversity, association study)

3.3. Identification and validation of candidate genes involved in constitutive expression of banana defence to *Mycosphaerella spp*, correlation with QTLs analyses

Peach

3.4. Characterization of the gene involved in the biosynthesis of 3,5-dicaffeoylquinic acid.

3.5. QTL mapping of biochemical components and traits linked to *Monilinia* resistance and of model parameters

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3.1. Characterization of the genetic diversity of plantains and cooking banana using genome-wide distributed molecular markers

The world's largest collection of cooking bananas and plantains is held in the field genebank of CARBAP in Cameroon. It will be characterized using the DArT technology. This will be performed in the DArT platform of the UMR DAP in Montpellier.

Output-> Identification of the population structure and diversity within bananas

3.2. Identification of candidate genes involved in the determination of cooking banana fruit quality traits (metabolic pathways, sequence and allelic diversity, association study)

•Identification of the metabolic pathways and of corresponding candidates genes underlying cooking banana major fruit quality traits (starch metabolism).

•Analysis of the sequence diversity of the candidate genes.

•Allelic diversity of candidate genes and association study on a large cooking banana collection.

•Transcriptomic approach. Analysis of the expression of the candidate genes at different stages during fruit development and starch accumulation will be performed for selected cooking banana and plantain genotypes with contrasting quality traits.

Output -> List, identification, differential expression, specific sequence polymorphisms of candidate genes

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3.3. Identification of candidate genes involved in constitutive expression of defense-related genes to *Mycosphaerella spp*, correlation with QTLs analyses

Based on preliminary studies constitutively expressed defences could play a role in Banana / *Mycosphaerella* interaction. Based on bibliographic data on banana, experiments on plant model and on WP2 results, the whole sequence of the banana A genome released in 2010 will allow to identify candidate genes. These candidates will start to be validated through a QRT-PCR approach in relation to plant resistance.

- Identification of candidate genes involved in constitutive expression of defense-related genes to *Mycosphaerella spp* in relation with WP2 results

- Validation of the genes through QRT-PCR approach in relation to plant disease level
- Correlation with QTLs analyses

Output -> List of candidate genes linked to banana defence to Mycosphaerella spp.

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3.4. Characterization of the gene involved in the biosynthesis of 3,5-dicaffeoylquinic acid, a phenolic compound compound toxic for aphid and involved in the resistance of Peach to *Myzus persicae*.

•A preliminary work for cloning the gene will be achieved according to a strategy based on the isolation and sequencing of the enzyme involved in the biosynthesis. The preliminary study will be conduct on *Ipomoea batatas* a plant species accumulating very high levels of 3,5-dicaffeoylquinic acid (up to 10% dry weight).

•The results obtained from this species will be helpful to start the characterization of the enzyme in peach and the cloning of the gene involved in the biosynthesis of the compound.

Output -> Characterization of the enzyme involved in the biosynthesis of dicaffeoylquinic acid in peach

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3.5. QTL mapping of biochemical components and traits linked to Monilinia resistance and of model parameters.

- An interspecific peach progeny (BC2) will be established in orchard in Avignon.
- Its genetic map will be made available and will allow a QTL mapping approach.

Output -> Genetic control of traits linked to Monilinia resistance in peach and model parameters for WP4.

4. Link WP2 and 3

Main scientific breakthroughs : to relate the biochemistry data to the understanding of the molecular basis of elaboration of fruit quality traits and plant defence.

The research question: can we identify a gene (or QTLs) coding for a key enzyme involved in the synthesis of specific biochemical compounds in our species of interest. The affirmative response to this question should help the breeders to select appropriate cultivars.

The availability of the Banana A genome sequence in 2010 will allow for the first time a large analysis at the genome scale leading to the identification of genes controlling Banana quality traits and defence to pathogens and, further on, to specific functional molecular markers that will increase breeding efficiency

An innovative approach is implemented in the project to handle the complex Peach/brown-rot system through an integrative view linking genetics, physiology, epidemiology and agronomy. The project will provide knowledge necessary to the cloning in different fruit species of the gene involved in the biosynthesis of a phenolic compound that shows interesting properties both for resistance to pest and pathogens and for human health.

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